APPLN. FILING DATE: JULY 10, 2001
TITLE: PEPTIDE SEQUENCES SPECIFIC...T LYMPHOCYTES
INVENTOR(S): GUERIN-MARCHAND AND DRUILHE
APPLICATION SERIAL NO: 010830-118 SHEET 1 of

SHEET 1 of 18



(5')	1	SDLEQERRAKEKLQEQQ
	18	SDLEQDRLAKEKLQEQQ
	35	SDLEQERLAKEKLQEQQ
	52	SDLEQERRAKEKLQEQQ
	69	SDLEQERRAKEKLQEQQ
	86	SDLEQDRLAKEKLQEQQ
	103	SDLEQERRAKEKLQEQQ
	120	SDLEQERKAKEKLQEQQ
	137	SDLEQERLAKEKLQEQQ
	154	SDLEQERRAKEKLQEQQ
	171	SDLEQERRAKEKLQEQQ
	188	SDLEQERRAKEKLQEQQ
	205	RDLEQ
	210	RKADTKKNLERKKEHGDILAEDLYGRLEIF
	240	AIELPSENERGYYIPHQSSLPQDNRGNSRD
	270	SKEISIIEKTNRESITTNVEGRRDIHKGHL
	300	EEKKDGSIKPEQKEDKS 316 (3')

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TITLE: PEPTIDE SEQUENCES SPECIFIC...T LYMPHOCYTES
INVENTOR(S): GUERIN-MARCHAND AND DRUILHE
APPLICATION SERIAL NO: 010830-118 SHEET 2 of

SHEET 2 of 18

(5') 1	AAAGCGATCTAGAACAAGAGAGGTGCTAAAGAAAGATTGCAAGAACAAC
52	AAAGCGATTTAGAACAAGATAGACTTGCTAAAGAAAAGTTACAAGAGCAGC
103	AAAGCGATTTAGAACAAGAGACTTGCTAAAGAAAAGTTGCAAGAACAAC
154	AAAGCGATCTAGAACAAGAGAGGGGGTGCTAAAGAAAAGTTGCAAGAACAAC
202	AAAGCGATTTAGAACAAGAGACGTGCTAAAGAAAAGTTGCAAGAACAAC
256	AAAGCGATTTAGAACAAGATAGACTTGCTAAAGAAAAGTTACAAGAGCAGC
307	AAAGCGATTTAGAACAAGAGACGTGCTAAAGAAAAGTTGCAAGAACAAC
358	AAAGCGATTTAGAACAAGAGACGTGCTAAAGAAAAGTTGCAAGAACAAC
409	AAAGCGATTTAGAACAAGAGACTTGCTAAAGAAAAGTTGCAAGAACAAC
460	AAAGCGATTTAGAACAAGAGACGTGCTAAAGAAAAGTTGCAAGAACAAC
511	AAAGCGATTTAGAACAAGAGACGTGCTAAAGAAAAGTTGCAAGAACAAC
562	AAAGCGATTTAGAACAAGAGACGTGCTAAAGAAAAGTTGCAAGAGCAGC
613	AAAGAGATTTAGAACAA
630	AGGAAGGCTGATACGAAAAAAATTTAGAAAGAAAAAAGGAACATGGAGAT
681	ATATTAGCAGAGGATTTATATGGTCGTTTAGAAATACCAGCTATAGAACTT
732	CCATCAGAAAATGAACGTGGATATTATATACCACATCAATCTTCTTTACCT
783	CAGGACAACAGAGGGAATAGTAGAGATTCCAAGGAAATATCTATAATAGAA
834	AAAACAAATAGAGAATCTATTACAACAAATGTTGAAGGACGAAGGGATATA
882	CATAAAGGACATCTTGAAGAAAGAAGATGGTTCAATAAAACCAGAACAA
936	AAAGAAGATAAATCT 950 (3')

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INVENTOR(S): GUERIN-MARCHAND AND DRUILHE

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RDELFNELLNSVDVNGEVKENILEESQVNDDIFNSLVKSVQQEQQ HNVEEKVEESVEENDEESVEENVEENDDGSVASSVEESI ASSVDESIDSSIEENVAPTVEEIVAPTVEEIVAPSVVEKCAPSVE **ESVAPSVEESVAEMLKER**

APPLN. FILING DATE: JULY 10, 2001 TITLE: PEPTIDE SEQUENCES SPECIFIC...T LYMPHOCYTES

INVENTOR(S): GUERIN-MARCHAND AND DRUILHE

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67T 6AG CAC AAG ACG TTG TTG TTG

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INVENTOR(S): GUERIN-MARCHAND AND DRUILHE APPLICATION SERIAL NO: 010830-118 SHEET SHEET 5 of 18

LSA-TER

7295-NRI 7295-NRII 7295-Rep

LEESQVNDDIFSNSLVKSVQQEQQHNV VEKCAPSVEESVAPSVEESVAEMLKER

DELFNELLNSVDVNGEVKENILEESQ

NSRDSKEISIIEKTNRESITTNVEGRRDIHK

APPLN. FILING DATE: JULY 10, 2001

TITLE: PEPTIDE SEQUENCES SPECIFIC...T LYMPHOCYTES

INVENTOR(S): GUERIN-MARCHAND AND DRUILHE

APPLICATION SERIAL NO: 010830-118 SHEET

NUCLEOTIDE SEQUENCE OF THE LSA GENE 5' END

(NON-CODING 5' END)

1 AAAGTATACATCTTCCTTCTTTACTTCTTAAA

(CODING 5' END, UNIQUE)

- 33 ATGAAACATATTTTGTACATATCATTTTACTTTATCCTTGTTAATTTATTG
- 84 ATATTTCATATAAATGGAAAGATAATAAAGAATTCTGAAAAAGATGAAATCA
- 135 TAAAATCTAACTTGAGAAGTGGTTCTTCAAATTCTAGGAATCGAATAAATGA
- 186 GGAAAATCACGAGAAGAAACACGTTTTATCTCATAATTCATATGAGAAAACT
- 237 AAAAATAATGAAAATAATAAATTTTTCGATAAGGATAAAGAGTTAACGATGT
- 288 CTAATGTAAAAAATGTGTCACAAACAAATTTCAAAAGTCTTTTAAGAAATCT

- 441 AAGGGCAAGACGAAAACAGACAAGAAGATCTTGAAGAAAAAGCA

(CODING 5' END, repetitive)

- 492 GCTAAAGAAAGTTACAGGGGCAACAAAGCGATTCAGAACAAGAGAGACGT
- 543 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTT
- 594 GCTAAAGAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
- 645 GCTAAAGAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTT
- 696 GCTAAAGAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
- 747 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
- 798 GCTAAAGAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGAC<u>T</u>T
- 849 GCTAAAGAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAGATAGACTT
- 900 GCTAAAGAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
- 951 GCTAAAGAAAGGTTGCAAGAACAACAAAGCGATTTAGA 988

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TITLE: PEPTIDE SEQUENCES SPECIFIC...T LYMPHOCYTES

INVENTOR(S): GUERIN-MARCHAND AND DRUILHE
APPLICATION SERIAL NO: 010830-118 SHEET 7 of 18

956 b.p. ATGAAACATATT ... AAGCGATTTAGA linear -> 1-phase Translation LSA.5'/ATG sequence DNA

AGA arg CAT his AAG 1ys CTT GAA glu GTT val AAG lys TTT TTG CAC his GAT asp AGT ser AAT asn ATA ile AAC asn AAA 1ys TTC AAA lys TTG leu TTA AAG 1ys TCT ser TTT phe TTC phe TTA AAA lys AAA lys GAG glu AAA 1ys AAT asn AAT asn ATA ile AAT asn AAT asn CAC his ACA thr AAT asn AAT asn CAA gln GAA glu ATC ile GTT val GAA glu GAA glu TCA ser AAA 1ys GAA glu CTT ATC ile GAT asp AAT asn GTG val CTT leu GAG glu AAT AAT asn AAA lys AAT asn TTT phe TTC GAA 51 51 ATA ile 71 AAA AAA 1111 ATA ile phe , 31 TCT ser CGA arg / ACT thr / GTA val / asn ser ' 91 AAT asn 151 AAT asn 211 211 1ys 271 271 AAT asn 331 GAG AAG 1 AGG arg GAG glu TCA ser ATA ile TAC tyr ATG met TCT TAT GTT val TTG leu ATA ile AAT asn TCA Ser ACG thr GGT ATT ile AAG 1ys TCA ser AAT asn TTA CTT leu AAA CAT
lys his
/ 21
AAT GGA
asn gly
/ 41
GGT TCT
gly ser
/ 61
TCT CAT
ser his
/ 81
AAA GAG
lys glu
/ 101
AGA AAT
arg asn 1 ATG Met 61 ATA ile 121 121 181 174 TTA 301 301 TTA 1eu

FIGURE 7A

666 gly

AAA 1ys

ATT ile

TAT

AAA lys

AAA 1ys

AAA 1ys

GAT asp

GAC asp

GAT asp

ATA ile

CAC his

GAA glu

TTA

AAG 1ys

GAA glu

AAA 1ys

GCT ala

GCA ala

AAA 1ys

GAA glu

GAA glu

CAA gln

AGA arg

AAC asn

CAA gln

GAA glu

CAA gln

TTG leu

AAG 1ys

GAA glu

AAA lys

GCT ala

CAA gln

GAA glu

TCA ser

GAT asp

APPLN. FILING DATE: JULY 10, 2001 TITLE: PEPTIDE SEQUENCES SPECIFICT LYMPHOCYTES INVENTOR(S): GUERIN-MARCHAND AND DRUILHE APPLICATION SERIAL NO: 010830-118 SHEET 8 of 18														
666	AGC	GAA	AGA	AAA	TTG									
81y	ser	glu	arg	1ys	1eu									
CAG	CAA	TTA	GAG	GCT	AAG									
gln	gln	leu	glu	ala	1ys									

CAA gln

GAA glu

TTA

GAT asp

AGC ser

CAA gln

CAA gln

GAA glu

GAA glu

AAA 1ys

GCT ala

CGT

CGT arg

AGA arg

GAG glu

CAA gln

GAA glu

TTA

GAT asp

AGC ser

CAA gln

TTG

AAG 1ys

GAA glu

GAA glu

AAA lys

GCT

CGT

AGA arg

GAG glu

CAA

GAA glu

CAA gln

CAA

GAA glu

CAA

GAT asp

AGC ser

CAA gln

CAA gln

GAA glu

CAA gln

TTG leu

AAG lys

AAT
asn
(CTT
leu
/
AAA
arg
/
Iys
/
TTG
leu
/
CAA
GAT
asp

CTT

AGA arg

GAG glu

CAA gln

121 171A 16u 16u 161 161 161 161 161 173 175 175

AAAA 1ys 1ys / GAC CAA CAA TTA 1eu / GGCT ala / AAG

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TITLE: PEPTIDE SEQUENCES SPECIFIC...T LYMPHOCYTES
INVENTOR(S): GUERIN-MARCHAND AND DRUILHE
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	CAG	glu	GAT	asp	•		
	GAG	ıgın glu	AGC	ser			
	CAA	gln	CAA	gln)	TTA	leu
	TTA	ln glu arg leu ala lys glu lys leu gl / 291	CAA	gln)	GAT	asp
	AAG	lys	GAA	glu)	AGC	ser
	GAA	glu	CAA	gln)	CAA	gln
	AAA	lys	TTG	leu		CAA	gln
	GCT	ala	AAG	lys		GAA	glu
	CTT	len	GAA	glu	ı	CAA	gln
	AGA	arg	AAA	lys	,	TTG	len
271	GAG	glu 291	CT 9	ala	311	AGG	arg
\	CAA	gln /	CTT	len	_	GAA	glu
811	GAA	glu 871	AGA	arg	931	AAA	lys
	TTA	leu glu gln 871 /	GAT	asp		CCT 6	ala
	GAT	ser asp	CAA	gln		CGT	arg
	AGC	ser	GAA	glu		AGA	arg
	CAA	gln	TTA	leu		GAG	glu
761	CAA	gln 281	GAT	asp	301	CAA	gln
\	GAA	glu /	AGC	ser	_	GAA	glu
/81	CAA	gln 841	CAA	gln	901	TTA	len

FIGURE 7C

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TITLE: PEPTIDE SEQUENCES SPECIFIC...T LYMPHOCYTES
INVENTOR(S): GUERIN-MARCHAND AND DRUILHE

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NUCLEOTIDE SEQUENCE OF THE LSA GENE 3' END

(CODING 3' END, REPETITIVE)

- 1 CAAGAACAACAAAGCGATCTAGAACAAGAGAGACGT
- 37 GCTAAAGAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGATAGACTT
- 88 GCTAAAGAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAGAGAGACTT
- 139 GCTAAGAAAGTTGCAAGAACAACAAAGCGATCTAGAACAAGAGAGACGT
- 190 GCTAAAGAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
- 241 GCTAAAGAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGATAGACTT
- 292 GCTAAAGAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAGAGAGACGT
- 343 GCTAAAGAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
- 394 GCTAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTT
- 445 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
- 496 GCTAAAGAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
- 547 GCTAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
- 598 GCTAAAGAAAGTTGCAAGAGCAGCAAAGAGATTTAGAACAA

(CODING 3' END, UNIQUE)

- 640 AGGAAGGCTGATACGAAAAAAATTTAGAAAGAAAAAAGGAACATGGAGAT
- 691 ATATTAGCAGAGGATTTATATGGTCGTTTAGAAATACCAGCTATAGAACTT
- 742 CCATCAGAAAATGAACGTGGATATTATATACCACATCAATCTTCTTTACCT
- 793 CAGGACAACAGAGGGAATAGTAGAGGATTCCAAGGAAATATCTATAATAGAA
- 844 AAAACAAATAGAGAATCTATTACAACAAATGTTGAAGGACGAAGGGATATA
- 895 CATAAAGGACATCTTGAAGAAAAGAAAGATGGTTCAATAAAACCAGAACAA 946 AAAGAAGATAAATCTGCTGACATACAAAATCATACATTAGAGACAGTAAAT
- 997 ATTTCTGATGTTAATGATTTTCAAATAAGTAAGTATGAGGATGAAATAAGT
- 1048 GCTGAATATGACGATTCATTAATAGATGAAGAAGAAGATGATGAAGACT
- 1099 TAGACGAATTTAAGCCTATTGTGCAATATGACAATTTCCAAGATGAAGAAA
- 1150 ACATAGGAATTTATAAAGAACTAGAAGATTTGATAGAGAAAAATGAAAATT
- 1201 TAGATGATTTAGATGAAGGAATAGAAAAATCATCAGAAGAATTATCTGAAG
- 1252 AAAAAAAAAAAGGAAAGAAATATGAAAAAACAAAGGATAATATTTA
- 1303 AACCAAATGATAAAAGTTTGTATGATGAGCATATTAAAAAATATAAAAATG
- 1354 ATAAGCAGGTTAATAAGGAAAAGGAAAAATTCATAAAATCATTGTTTCATA
 1405 TATTTGACGGAGACAATGAAATTTTACAGATCGTGGATGAGTTATCTGAAG
- 1456 ATATAACTAAATATTTTATGAAACTATAA (stop)

(NON-CODING 3' END)

1485 AAGGTTATATATTT 1498

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TITLE: PEPTIDE SEQUENCES SPECIFIC...T LYMPHOCYTES INVENTOR(S): GUERIN-MARCHAND AND DRUILHE

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LSA.3'.ALL -> 1-phase Translation

CAAGAACAACAA ... GGTTATATATTT linear 1496 b.p. DNA sequence

CGT arg CAA gln GAT asp GAA glu CAA gln CAA gln GAA glu AAA lys TTG leu GAA glu AGC AGA arg ser CAA gln CAA gln CTA leu AAG lys GAG glu GCT ala GAT asp GAA glu TTG leu CAA gln CAG gln CTT AAG lys AGA arg GAG glu AGC ser GAA glu AAA lys GAA glu CAA gln CAA gln GAT asp TTA GCT ala GAT AAA lys CAA gln CGT arg TTA CAA gln AGA arg GCT ala AAG 1ys GAA glu GAA glu AGC ser GAG / GAA glu CAA gln TTA CGT CAA gln AGA arg CAA gln AAA lys TTG GAT asp CAA gln GAG glu AAG 1ys AGC ser GAA glu GCT ala GAA glu / 11 GAA CAA glu gln glu gln
/ 31
AGA CTT
arg leu
/ 51
AAA GAA
lys glu
/ 71
TTG CAA
leu gln
/ 91
CAA CAA
gln gln
/ 111
GAT TTA 31 CTA leu 91 GAT asp 151 151 GCT ala 211 1ys 271 GAA GAA 81u 331 AGC GAT asp GAA glu CAA gln CAA gln CAA gln CTT AGA arg AGC ser GAA glu AAA lys TTG leu CAA gln TTA GAG glu GCT ala AAG 1ys GAA CAA glu gln / 21 AGC GAT ser asp / 41 GAA CAA glu gln / 61 AGA CGT arg arg / 81 AAA GAA lys glu / 101 TTA CAA

CAA CCAA ggln GAT CGT CGT CGT CGT CGT CGT Ileu / ATA ile

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FIGURE 9B

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TITLE: PEPTIDE SEQUENCES SPECIFIC...T LYMPHOCYTES
INVENTOR(S): GUERIN-MARCHAND AND DRUILHE

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	AAA	lys			ser		CAA	gln)	GAA	glu)	GAT	asb	-	TTA	leu		AAA	lys ile lys
	CAT	his			lys			phe	-	GAA	glu)	CAA	gln)	AAT	asn		ATA	ile
	ATA	ile		GAT	asp	•		asp		GAT	asb	-	TTC	phe	-	GAA	glu)	AAA	lys
	GAT	asp		GAA	glu)	AAT	asn		ATA	ile		AAT	asn		AAT	asn		GAA	glu
	AGG	arg asp ile h		AAA	lys glu		GTT	Val		TTA	leu ile asp		GAC AAT	asp	•	AAA	lys	•	GAA	nlg
	CGA	le thr thr asn val glu gly arg ar		CAA	gln	•	GAT	asp	•	TCA	ser		TAT	tyr		GAG	glu)	TCT	ser
	GGA	gly		GAA	glu)	TCT	ser		GAT	asp	•	CAA	gln	•	ATA	ile		TTA	glu glu leu s
	GAA	glu		CCA	pro		ATT	ile		GAC	asp	•	GTG	val		TTG	leu		GAA	glu
	GTT	val		AAA	lys		AAT	asn		TAT	tyr	1	ATT	ile		GAT	asp	•	GAA	glu
	AAT	asn		ATA	ile		GTA	val		GAA	glu	,	CCT	pro		GAA	glu		AAA TCA TCA G	ser
	ACA	thr		TCA	ser		ACA	thr	1	GCT	ala		AAG	lys		CTA	leu	_	TCA	ser
291	ACA	thr	311	GGT	gly	331	GAG	glu	35.	AGT	ser	37]	E	phe	39.	GAA	glu	411	AAA	lys
	⋖			GAT	asp	_	TTA	leu	/ 1	ATA	ile	/ 1	GAA	nlg	\ _1	AAA	lys	/]	ATA GAA	glu
871	TCT	Ser	931	AAA	lys	991	ACA	thr	1051	GAA	glu	1111	GAC	asp	1171	TAT	tyr	1231	ATA	ile
	GAA				lys		CAT	his		GAT	asp		TTA	len		ATT			66A	
	AGA	arg		GAA	glu		AAT	asn		GAG	glu		GAC	asp		GGA	gly		GAA	glu
	AAT	asn		GAA	glu		CAA	gln	_	TAT	tyr		GAA	nlg		ATA	ile	_	GAT	asb
281	ACA	thr	301	CT	len	321	ATA	jle	34.	AAG	lys	36.	GAT	asp	38.	AAC	asn	40.	TTA	len
\	AAA	lys	\	CAT	his	\	GAC	asp	<u> </u>	AGT	ser	/ 1	GAT	asp	/ 1	GAA	glu	/ 1	GAT	asp
841	GAA	glu	30T	66A	gly	961	CCT	ala	102	ATA	ile	108]	GAA	glu	114]	GAA	glu	1201	GAT	asp

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TTG GAT AAA 1ys GAA glu AGT ser GTG val AAA AAG 1ys ATC ile TAT GAT GAA glu CAG gln AAT asn AAG lys TTA GTT val CCA / AAT asn ATT ile AAG lys AAA 1ys TAA 0CH GTT val GAA glu CTA leu CAG gln AAT asn phe GAC AAA 1ys AAG 1ys asn AAT 431 AAG GAT AAT / ATG met GAT GGA gly lys asp 451 AAA AAT lys asn 471 TTT asp GAC GAA glu phe GAT asp tyr leu AAG AAA lys lys 441 GAG CAT glu his 461 AAA TCA lys ser 481 GAA 1261 / AAA GGA lys gly 1321 / TAT GAT tyr asp 1381 / TTC ATA phe ile 1441 / GAG TTA glu leu

FIGURE 9D

APPLN. FILING DATE: JULY 10, 2001

TITLE: PEPTIDE SEQUENCES SPECIFIC...T LYMPHOCYTES INVENTOR(S): GUERIN-MARCHAND AND DRUILHE

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LSN.3'STOP -> 1-phase Translation

CAAGAACAACAA ... ATGAAACTATAA linear b.p. 1482 seduence DNA

GAA gln CGT GAA glu GAT asp CAA gln CAA gln AGA arg GAA glu GAA glu AAA 1ys AGC ser CAA gln CAA gln CTA leu GAG glu AAG lys GCT ala GAA glu TTG leu CAA gln CAG gln GAT asp CTT leu AGA arg GAA glu AAA lys AAG 1ys GAG glu AGC ser GAA glu GAT asp CAA gln CAA gln TTA AAA lys GAT asp CAA gln CAA gln TTA CGT arg AAG 1ys GCT ala GAA glu AGC ser GAA glu AGA arg GAA glu CAA gln CGT TTA GAG glu CAA gln AGA arg AAA 1ys CAA gln TTG leu CAA gln GAT asp GAG glu GAA glu GAA glu AGC ser AAG lys GCT ala CTT 1eu 51 CAA GAA 631 CAA 631 AGA arg AAA 1ys TTG leu / CAA gln GAT asp 31 CTA 1eu 91 GAT asp 151 151 GCT AGG 1ys 271 GAA GAA 81u 331 AGC GAT asp CAA gln CTT leu GAA glu CAA gln CAA TTG AGC ser GAA glu AGA arg AAA lys CAG CAA gln TTA GAG glu GAG glu AAG lys GCT ala GAT asp 41 CGT CGT arg 81 GAA GAA GIU 101 CCAA GIN GAA GAA Blu / AGA arg / AAA lys TTA ser

FIGURE 10A

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				-						-				_						-		
	CAA	gln	TTA	leu))	GAG	glu	; ;	GCT	ala		AAA	1 / 5	,	TTA	1611	; ;	CAA	ฮไท	:	ATA	ile
	CAA	gln	GAT	asp	<u>-</u>	CAA	ยไท	5	CGT	arg)	AAA	1 \ S		<u> 190</u>	arg	0	CAT	his) •		ile
		glu	AGC	Ser	• •	GAA	glu	5	AGA	arg)	ACG	thr	;	GGT	81V		CCA	pro	_		ser
	CAA	gln	CAA	ยไท	.	TTA	leu		GAG	glu)	GAT	asp	<u>L</u> 1	TAT	tvr		ATA	ile		ATA	ile
	TTG	len	CAA	gln)	GAT	asp	-	CAA	gln)	GCT	ala	; ;	TTA	leu		TAT	tvr	,	GAA	glu
	AAG	lys	GAA	glu)	AGC	ser		GAA	glu)	AAG	1 \ S		GAT	asp	-	TAT	tvr	,	AAG	lys
	GAA	nlg	CAA	gln)	CAA	gln)	TTA	leu		AGG	a g		GAG	glu)	GGA	gly	,)	TCC	ser
	AAA	lys	TTG	leu		CAA	gln)	GAT	asp	•	CAA	gln	·	GCA	ala		CGT	a g)		asb
	GCT	ala		lys	•		glu		AGC	ser		GAA	glu)	TTA	leu			glu)	AGA	arg
•		arg	GAA	glu)	CAA	gln)	CAA	gln	l	TTA	leu		ATA	ile		AAT	asn		AGT	ser
	AGA	arg	AAA	lys	•	TTG	leu		CAA	gln		GAT	asp	-	GAT	asp	-	GAA	glu	•	AAT	asn
131	GAG	glu 151	GCT	ala	171	AAG	lys	191	GAA	glu	211	AGA	arg	231	GGA	gly	$\overline{251}$	TCA	ser	271	999	gly
\	CAA	gln /	CTT	leu	_	GAA	glu	_	CAA	gln	\	CAA	gln	`	CAT	his	_	CCA	pro	_	AGA	arg
391		glu 451	AGA	arg	511	AAA	lys	571	TTG	len	631	CAG	gln	691	GAA	glu	751	CTT	len	811	AAC	asn
	TTA								AAG									GAA			GAC	
		asb																			CAG	gln
		ser																			CCT	
		gln 141																				
		gln /																				
361	GAA	glu 421	AGC	ser	481	GAA	glu	541	AGA	arg	601	AAA	lys	661	AAT	asn	721	GAA	glu	781	TCT	ser

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INVENTOR(S): GUERIN-MARCHAND AND DRUILHE
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													_					-		
	AAA lys		ser	;	CAA gln	5	GAA	glu	1	L YS	asb	i	∀ .	len	< <	AAA	lys	(-	<u>5</u>	1911
	CAT his	A A A	lys	<u>+</u>	phe	<u> </u>	GAA	glu	•	, }	gln	ŀ	AAI	asn			ile			
	ATA ile	TΦ	asp	F <	asp			asp	(}	ر - 	bhe			n1g	< < <	777	lys	< < <	אאא אפן	[VS
	GAT		nlg glu	F <	asn		ATA	leu ile		A .		F	- F	asn	\ \ \ \	7	glu	F < 0	ב כ	asp
	AGG arg		lys		val		TTA	len	(שאר הייני	asb		ל ל ל ל				glu			
	CGA arg		gln	7∆7	asp		TCA	ser	TAT	- ; - ;	Lyr	7	ָבָּלְ בַּלְּבָּלְ	ر ا ا			ser	ر ر _۵	ָּ ֖֭֓֞֞֞֝֞֝֞֝֓֞֝	pro
	GGA gly	GAA	glu	TCT	ser			asb	Δ Δ Δ	ל ל נ	20	ΔΤΔ	<	ט -	TTA	<u> </u>	ren			
	GAA		pro		ile			asb		2 - 2			2 -		GAA		n 1 8	TTT		pue
	GTT val		lys	AAT	asn		I V		ATT	- <u> </u> -) - - -	GAT	200	<u>2</u> 3	GAA	; ;	2 2 2	AAT	2	d N
	AAT asn		ile		val		GAA	ာ ၂ ၈	CCT	ה ה	<u>.</u>	GAA	= [b	۵ 2	TCA	. L	ב	AAT	2	<u>م</u>
	ACA		ser	ACA	thr	1	۔ ر	ala 1	AAG	7 \	ני	CTA] e I	411	TCA		מ	GAT	מטמ	۵ 5
	ACA thr 311		gly 331		glu	35	AGI	3er 371	Ë	phe	39,	. AS	glu	411	AAA	7 \ \ \ \ \	431	AAG GAT	1 \ \ \ \	ر ر د
	All ile	GAT	lys asp 991 /	TTA	leu	/ T	A :	1 Le	GAA	glu	7	AAA	ΊVS	/	GAA	α] ::	ر م	ACA	thr	=
871		AAA	1ys 991	ACA	thr	105	֡֝֞֝֝֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓	2.c	GAC	asp	117	TAT	tyr	1233	ATA	q	1291	AAA	7 \	,
	glu glu	AAG	lys	CAT	his	ΤΔ.	י ע עם ני	a v U	TTA	leu		ATT			GGA			GAA		
	arg	GAA		AAT				219				GGA	gly	!	GAA	מות	5	TAT	tvr	. 6
	asn .	. GAA	n] &	CAA	gln	± TAT	+ × +	1 1	GAA	glu	~	ATA	ile	-	GAT	asp	-	AAA	ľys	, >
281 ACA	thr 301	L				AAG	1 \ \	36	GAT	asp	38	AAC	asn	40	TTA	leu	42.	AAG	lys	,
L AAA	1ys	CAT	sru /	. GAC	asp 1	, AGT	200	1 /	GAT	asp	1 /	GAA	glu	1	GAT	asb	. /	66A	gly	•
841 GAA	g1u 901	GGA	8 L y 961	GCT	a La 107	ATA	1.1P	108	GAA	gln	114	GAA	glu	120.	GAT	asb	126	AAA ,	Lys	

FIGURE 10C

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AAA lys GAT GAA glu GTG val AAG 1ys ATC ile TAT GAA glu CAG gln ATA ile AAG lys TTA GTT val AAT asn AAG lys GTT val GAA glu TAA OCH CAG gln AAT asn CTA AAG 1ys AAA 1ys GAC asp GAT asp ATG met GGA gly asn GAC asp TTT AAA 1ys TTT phe ATA ile GAT asp leu GAA ser

FIGURE 10D